



Structure of HTPL and alignment of Patched motifs.

FIG. 1A

HTPL-L (954 a.a.)



HTPL-S (767 a.a.)



Patched

FIG. 1B

Patched motif

Consensus	1	VLSSKIRYTFPPDDIRSYTERGSRSEHEPL-VERKFFPGDGYPISRFSIITAKARNS-NILDIRVLNEVQVNDPISTNV	78
HTPL-L	162	deeedleehyTPVGPSPAKAERRFVQGHFTTnDSYRFSASRRSTEANFVSLLVSYSD-SLLDPATFAEVSKLDGAVQDLR	240
gi 1825729	47	NPLSDAVLFTPLGAQSKMERMSIHEKWPL-TDNNYIPGRAVTSQREIQVTALARNDsNILDPKANAVYQLDKYIQTRV	125
gi 1707052	22	NVVSLLMTIFGPY---SYTERRIIHDAWPL-VDGTFVAGRAVTSQREIQVAVVARGGnILDRVFSNELKLMESFIRNNI	97
gi 3892144	49	LRVDDPSYVFTPSDARWRREISVFENENWPL-DENKFLPGKSFEAKRFVNILIRAKDGGsIMRDNVlHEIEILNQWIMNNI	127
Consensus	79	TIPVSG--ITLSFKDLCMRFCDCINCPVNQHYNGQILRSNlHNSRIDLTYPMTFFGTKIYLGNPFGGVKLDPN---	152
HTPL-L	241	VAREKG---SQIQYQQVCARYALCPNPILYAWQVKNKTLNLS--SISFPAYNHGRHPLYLGTGFFGYILGGS---	313
gi 1825729	126	RVLHNG--HYYSYKNLCLQYKNGGCCPSNKHV---HILSDLHNHGPNITYPYFRPGSEGGYIGSSIAGGVTVMKgenetDI-	199
gi 1707052	98	TVQFSN--RTWSFADLCLAGpDGRCANNDHI---QLASRLHQHGPNITYPTVRLSDKSAYIASAIGGVKLAKgdngeNI-	171
gi 3892144	128	SIPTDDIkFNLTYQDLCLSY-DWVCGANEHIQ-MLLRRNDVNQILDHFPRGGTKDTPVYLGGIGFDVQFFQn---GT-	200



FIG. 1B

Patched motif (Continued)

	170	180	190	200	210	220	230	240	
consensus	153	154	155	156	157	158	159	160	226
HTPL-L	161	162	163	164	165	166	167	168	227
gi 1825729	169	170	171	172	173	174	175	176	228
gi 1707052	177	178	179	180	181	182	183	184	229
gi 3892144	185	186	187	188	189	190	191	192	230
	250	260	270	280	290	300	310	320	
consensus	227	228	229	230	231	232	233	234	293
HTPL-L	235	236	237	238	239	240	241	242	294
gi 1825729	243	244	245	246	247	248	249	250	295
gi 1707052	251	252	253	254	255	256	257	258	296
gi 3892144	259	260	261	262	263	264	265	266	297
	330	340	350	360	370	380	390	400	
consensus	294	295	296	297	298	299	300	301	370
HTPL-L	302	303	304	305	306	307	308	309	371
gi 1825729	310	311	312	313	314	315	316	317	372
gi 1707052	318	319	320	321	322	323	324	325	373
gi 3892144	326	327	328	329	330	331	332	333	374
	410	420	430	440	450	460	470	480	
consensus	371	372	373	374	375	376	377	378	416
HTPL-L	379	380	381	382	383	384	385	386	417
gi 1825729	387	388	389	390	391	392	393	394	418
gi 1707052	395	396	397	398	399	400	401	402	419
gi 3892144	403	404	405	406	407	408	409	410	420



FIG. 1B

Patched motif (Continued)

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consensus 417 490 500 510 520 530 540 550 560
HTPL-L -----SSKSHE--AEQ--AVKFFFLNLYCPFLNPKVRVCVLIVLVYLAIAIYGCNTMKEGLDPAKL 475
gi 1825729 469 -----SVPDEHgtDIH--PMSLFRRDYFGPFLTRSESKEYFVFIYLYIISSYVGCFFHVQEGDLRNL 632
gi 1707052 451 -----HSASHD--VKOp-LTSRFFGEWYAPVLMHPVVRGIAMVWFYIYLLGASVGCSSRIKEGLEPVNL 528
gi 3892144 515 -----tssvstmtsqtSPASKH--LHHC-AATSFRRWYAPVLMQPIWIRAIAGLWLIYLGISYVGCSTHLKEGLEPANL 522
gi 3892144 515 ipaefawkeqgspnsslSKSKD--REEKdRIVHFIGIKTYGPFILNSVRIFSGLIFFVYLAIAMVGCYNFREGNPGNL 592

consensus 476 570 580 590 600 610 620 630 640
HTPL-L -----FLKDSPLVEYLRLREKHVWPYGLQVTVFNNPPDLTNPENRDLNEMVDEFENPYAMGKNSTKFWLRDYNFLYSFISE 555
gi 1825729 529 -----LVEDSYAI PHYRLLeKYFWYQQQVQIVINNAPDLRNHTSRDRVHAMVLDFAISKHAIGMESVQFWLFEMER--YVQKELE 709
gi 1707052 523 -----LVDDSYATPHYRVLeKHYWHYGASLQIVVSNPPDLRDPVERINMDKMASTFANCKVAIGDSSVQFWLREMQ--VSEEHK 600
gi 3892144 593 -----VTNDHYIAKYFSDI--KHFWRIGAQLHVAVLNPPNLTISENRNELLKVVSAFENTQYTLGREGTVFLLLEYLNLSELNAE 671

consensus 556 650 660 670 680 690 700 710 720
HTPL-L -----LEDEEEEFYDLEWFL--KSPGFSHWVGDLVWDN--KTDYETTVIVKKFRFTGGKDLSTWTDRLTKTWRGVADEYPDFN 633
gi 1825729 608 -----VQIID--SSFYGLLHHFL--ASKTNNPLAEDIYWGpPDDNDGTWVKSFRFILGMDLVTMDQTDATMSFREVAARWPEFN 685
gi 1707052 601 -----IQYDN--EKFYDHAAQYI--YSDMSQPWWVDVWVG--RNNNSERI IKTFRFMIGMRDISTTTKQTEATNTFREIASRFEQYN 676
gi 3892144 672 -----VEDTERLWKTKLNSWLK--YTGGSQTQWASNLKIN-----KTDGSFQAFRFQIALKNFVEPNHDKHAAQLLRDIADHP--FN 744

consensus 634 730 740 750 760 770 780 790 800
HTPL-L -----VTVFDE-----APFLDQILSIGPTTIQSIITWTLICMAVVCFLFIPNPTVFVITVSI 686
gi 1825729 686 -----LMVYNQA-----FIYFDQYAAILEDVTRNVLVASAAMFIVSLLIIPYPLCSLWVTFAI 832
gi 1707052 677 -----VTTFMPI-----WMFTDQYIIIIIPNTVQNIITALLVMIVIAVLFIPOPMCSLWVALAC 738
gi 3892144 745 -----VVTYMP-----WLFTDQYALVVPNTMQDIIIVAVACMLVISALLIIPQVCSFWAVTI 729
gi 3892144 745 VVYHEVsfgnrkilndfisschscyaqknipklaFPFADQYLIILPATIQNVVISLLCMVAVSFLIVPSLPSGFVIFVSI 824
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FIG. 1B

Patched motif (Continued)

	810	820	830	840	850	860	870	880	
consensus*.....*.....*.....*.....*.....*.....*.....								
HTPL-L	687 ASIDIGVFGFLSLWGVLDLPISMITITIMSIGFSVDPSAHIAHYFVRSHGSETPDERLADALEALGWPIQAAALSTILCVL	766							
gi 1825729	833 GSVIVGVTFGMAFWKVNLDLSISMINLVICTGFSFDSAHISYAFV-SSSQPSVNQKSVEALYLLGYFVLPVLSAISTIIIGVC	911							
gi 1707052	739 ASIDFGVIGYMTLWGVNLDLSISMITITIMSIGFSVDPSAHIAHYGVVVSRED-TAAGRKVEALSALGWPLSQGAMSTIIAVS	817							
gi 3892144	730 GSIDLGVLGFMFLWNVNLDLSISMITITIMSVGFSVDPSAHITVAVVISKES-TTSARVCDALGDLGWPAQAGAMSTILAVS	808							
	825 VSINIGVFGYMTLWGVNLDLSISMITITIMSIGFAVDLSAHIIYAFVTSHG--DTKQRVIGALETILGWPIFQGASSTIAGIS	902							
	890	900	910	920	930	940			
consensus*.....*.....*.....*.....*.....*.....*.....								
HTPL-L	767 PLLFVPSYVMVVFVKTIPLVGVVIGLHGLIFLPIILSLFVT-----IRTSNAKIKKPSSI	821							SEQ ID NO: 4805
gi 1825729	912 VLAAAKAYIFRTFFKIMFLVMIFGAHGLIFIPVFLTFGRfi-----	954							SEQ ID NO: 4806
gi 1707052	818 VLADIPAYMIVTFFKTVVLSISLGLHGLVFLPVLISIFVRGCCIIIPSSPHGPSAQKIEKQIRI	882							SEQ ID NO: 4807
gi 3892144	809 VLSDVPAYMIVTFFKTVFLAISIGFLHGLVFLPLMLSVFVGki-----fdIHISNISIKYCIYL	867							SEQ ID NO: 4808
	903 ILYTVDAYIILVFFKTIWLTLIGAIHGLFFIPIPLSLFPV-----EFFRIPKSSEL	954							SEQ ID NO: 4809



Structure of HTPL and alignment of Patched motifs.

FIG. 1A

HTPL-L (954 a.a.)



HTPL-S (767 a.a.)



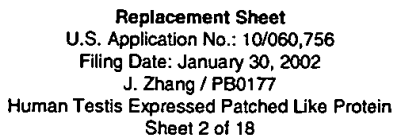
FIG. 1B

Patched motif

Patched

Consensus 1 VLSSKIRYTFPDDIRSYTERGSRSEHEPL-VERKFFPGDGYPISRFSIITAKARNS-NILDIRVLNEWQVNDFFISTNV 78
HTPL-L 162 deeedleehyTPVGSPPAKAERRFVQGHFTThDSYRFSASRRSTEANFVSLVVSYS-LLDPATFAEVSKLDGAVQDLR 240
gi 1825729 47 NPLSDAVYLFPLGAQSKMERMSIHEKWPL-TDNNYIPGRAVTSREIQVTALARNDSNILDPKFANAVYQLDKYIQTRV 125
gi 1707052 22 NVVYSLLMIFGPY--SYTERRIIHDAWPL-VDGTFVAGRAVTSREIQVAVVARSGNILDVFSNELKLMESIRNNI 97
gi 3892144 49 LRVDPPSYVFTPSDARWRREISVFNENWPL-DENKFLPKGSFEAKRFVNILIRAKDGgSIMRDNVILHEIEILNQWIMNNI 127

Consensus 79 TIPVSG--ITLSFKDLCMRFCDINCPVNOHYNGQILRSNLHNSRIDLTYPMTFFGTKIYLGPNFGVKLDPN---PGN- 152
HTPL-L 241 VAREKG--SQIQYQQVCARYALCVPPNPILYAWQVKNKTLNLS--SISFPAYNHGRHPLYLTFPGGYILGGS---LGMg 313
gi 1825729 126 RVLHNG--HYYSYKNLCLOYKNGGCPSNKHV---HILSDLHNHGFNITYPYFRFSGEGGYIGSSIGGVTVMKgeneTDI- 199
gi 1707052 98 TVQFSN--RTWSFADLCLAGpDGRCANNDHI---QLASRLHQHGINTITYPTVRLSDKSAYIASAIGGVKLAKgdngeNI- 171
gi 3892144 128 SIPTDDlkFNLTyQDCLSY-DWVCGANEHIQ-MLLRNDVNQILDHFRGGTKDTPVYLGGIPIGDVQFFQn----GT- 200



Patched motif (Continued)

consensus	153	170	180	190	200	210	220	230	240
HTTPL-L	314	170	180	190	200	210	220	230	240
gi 1825729	200	170	180	190	200	210	220	230	240
gi 1707052	172	170	180	190	200	210	220	230	240
gi 3892144	201	170	180	190	200	210	220	230	240
consensus	227	250	260	270	280	290	300	310	320
HTTPL-L	393	250	260	270	280	290	300	310	320
gi 1825729	274	250	260	270	280	290	300	310	320
gi 1707052	247	250	260	270	280	290	300	310	320
gi 3892144	275	250	260	270	280	290	300	310	320
consensus	294	330	340	350	360	370	380	390	400
HTTPL-L	453	330	340	350	360	370	380	390	400
gi 1825729	341	330	340	350	360	370	380	390	400
gi 1707052	314	330	340	350	360	370	380	390	400
gi 3892144	355	330	340	350	360	370	380	390	400
consensus	371	410	420	430	440	450	460	470	480
HTTPL-L	530	410	420	430	440	450	460	470	480
gi 1825729	418	410	420	430	440	450	460	470	480
gi 1707052	391	410	420	430	440	450	460	470	480
gi 3892144	435	410	420	430	440	450	460	470	480



FIG. 1B

Patched motif (Continued)

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consensus 417 490 500 510 520 530 540 550 560
HTPL-L -----SSKSHE--AEQ--AVVKFFLLNYCPFLLPKVRVCVLLVVLVYLAIAITGCTNMKEGLDPAKL 475
gi 1825729 572 -----SVPEHgtDIH--PMSLFFRDYFGPFLTRSESKYFVVFVIVLYIISIIYGCFFHVQEGDLRNL 632
gi 1707052 469 -----HSASHD--VKQP-LTSRFFGGEWYAPVLMHPVVRGIAMVWFVYLLGASVGCSSRIKEGLEPVNL 528
gi 1707052 451 -----tssvstmtsqatSPASKH--LHHC-AATSFRRWYAPVLMQPIRAIAGLWYLIYLGISITGCTHLKEGLEPANL 522
gi 3892144 515 ipaefawkeqgspnsslSKSKD--REEKDRIVHFIFIGKIYGPFILSNSVRIFSGLIFFVYLAIAIAMYGCYNFREGNPGNL 592

consensus 476 570 580 590 600 610 620 630 640
HTPL-L -----FLKDSPLVEYLRLREKHVWPYGLQVTFVNNPPDLTPENRDRLENMVDDEFENTPYAMGKNSTKFWLRDYENFLYSFISE 555
gi 1825729 633 ASDDSYITPYFNVEENYFSYGPVRVMVIVTKKVDYWDKVRQKLENTKIFEKNVY--VDKNLTFEVLDAYVQYLK--GNS 709
gi 1707052 529 LVEDSYAIPHRYLLeKYFWKYGQQQVQIVINNAPDLRNHTSRDRVHAMVLDFAFATSKHAIGMESVQFVLFEMER--YQKELE 607
gi 1707052 523 LVDDSYATPHYRVLeKHYWHYGASLQIVVSNPPDLRDPVERINMDKMASTFANCKVAIGDDSVQFVLRMQ--VSEIHK 600
gi 3892144 593 VTNDHYIAKYFSDI-KHFWRIGAQLHVAVLNPPNLTISENRNELLKVVSAPENTQYTLGREGTVFFLLELYNLSELNAE 671

consensus 556 650 660 670 680 690 700 710 720
HTPL-L -----LEDEEEEFYDILLEWFL-KSPGFSHWVGDLVWDN-KTDYETTIVKKFRFTTGGKDLSTWDRTRLLKWTWGVADYEPDFN 633
gi 1825729 710 QDPNEKNTFMNIPDFLsNFPNFQH-----DI-NISSNEIISRGF-IQTTDVSSSAKKKILLFQLRRIA-EDCQIP 779
gi 1707052 608 VQIID-SSFYGLLHHFL-ASKTNNPLAEDIYWGpPDDNDGTMVKSFRFILGMDKDLVTMDQTDATMSFREVAARWPEFN 685
gi 1707052 601 IQYDN-EKFDHAAQYI-YSDMSQPWVVDVWVG--RNNNSERIIKTFRFMIGMRDITSTTKQTEAENTFREIASRFEQYN 676
gi 3892144 672 VEDTERLWTKLNSWLK-YTGGSTQWASNLKIN-----KTDGSFQAFRQIALKNFVEPNDDHKHAAQLLRDIADHQP-FN 744

consensus 634 730 740 750 760 770 780 790 800
HTPL-L -----VTVFDED-----AFLDQILSIGPTTIQSIITWTLICMAVVCFLFIPNPTVFTVTSI 686
gi 1825729 780 LMVYNQA-----FIVFDQYAAILETVNRNLVASAAMFIVSLLLIPIYPLCSLWVTFAI 832
gi 1707052 686 VTFMPI-----WMFTDQYIIIIIPNTVQNIILVVMIVIAVLFIPQPMCSLWVALAC 738
gi 1707052 677 VTYMPL-----WLFQDQYALVVPNTMQDIIIVACMLVISALLIIPQVCSFWAVTI 729
gi 3892144 745 VVYHEVsfgnrkilndfisschscyaqknipklafPPADQYLIILPATIQNVVISLLCMAVVSFLIIVPSLPSGFVIFVSI 824
```



FIG. 1B

Patch d motif (Continued)

	810	820	830	840	850	860	870	880	
consensus*.....*.....*.....*.....*.....*.....*.....*.....*.....								
HTPL-L	687	ASIDIGVFGFLSLWGVLDLPISMITIIMSGFSVDFSAHIAHYFYSRSHGSETPDERLADALEALGWPIQAALSTILCVL	766						
gi 1825729	833	GSVIVGVTFGMAFWKVNLDSDISMINLVICTGFSDFSAHISYAFV-SSSQPSVNQKSVREALYLLGYVPLQSAISTIGVC	911						
gi 1707052	739	ASIDFGVIGYMTLWGVNLDALSMITIIIMSGFSVDYSAHIAHYGVVSRD-TAAGRVKEALSALGWPLSQGAMSTIIAVS	817						
gi 3892144	730	GSIDLGVLGFTLWNVNLDALSMITIIIMSVGFSVDYSAHITVAVVISKESTTSARVCDALGDLGWPAQGAMSTIIAVS	808						
gi 3892144	825	VSINIGVFGYMTLWGVNLDVSMISIIIMSGFAVDLSAHIIVAFVTSHG-DTKQRVICALETGLGWPIFGASSIIAGIS	902						
	890	900	910	920	930	940			
consensus*.....*.....*.....*.....*.....*.....*.....*.....*.....								
HTPL-L	767	PLLFVPSYVNVFFKTIPLVGVVIGLLHGLIFLPILSLFVT-----IRTSNAKIKKPSSI	821						SEQ ID NO: 4805
gi 1825729	912	VLAARAYIFRTFFKIMFLVMIFGAHGLIFIPVFLTFGRfi-----	954						SEQ ID NO: 4806
gi 1707052	818	VLADIPAYMIVTFFKTVLSLSGLLHGLVFLPVLLSIFVRGCCIIpsphGHPsAQIEKQIRI	882						SEQ ID NO: 4807
gi 3892144	809	VLSDVPAYMIVTFFKTVFLAISIGFLHGLVFLPLMLSVFVGki-----fdIHISNISIKYCIYL	867						SEQ ID NO: 4808
gi 3892144	903	ILYTVDAYIILVFFKTIWLTMLIGAIHGLFFIPIFLSLFPV-----EFFRIPKSSEL	954						SEQ ID NO: 4809